RAW SEQUENCE LISTING   DATE: 03/23/2001
PATENT APPLICATION: US/09/435,770   TIME: 16:39:39

Input Set : A:\Yamamto1.app
Output Set: N:\CRF3\03232001\I435770.raw

```
   4  <110> APPLICANT: YAMAMOTO, Takuo
   5         MARUTA, Kazuhiko
   6         KUBOTA, Michio
   7         FUKUDA, Shigeharu
   8         MIYAKE, Toshio
  10  <120> TITLE OF INVENTION: NON-REDUCING SACCHARIDE-FORMING ENZYME,
  11         TREHALOSE-RELEASING ENZYME, AND PROCESS FOR PRODUCING
  12         SACCHARIDES USING THE ENZYMES
  14  <130> FILE REFERENCE: YAMAMOTO=16A
  16  <140> CURRENT APPLICATION NUMBER: 09/435,770
  17  <141> CURRENT FILING DATE: 1999-11-08
  19  <150> PRIOR APPLICATION NUMBER: JP 258,394/1998
  20  <151> PRIOR FILING DATE: 1998-09-11
  22  <150> PRIOR APPLICATION NUMBER: JP 352,252/1998
  23  <151> PRIOR FILING DATE: 1998-12-11
  25  <150> PRIOR APPLICATION NUMBER: JP 16,931/1999
  26  <151> PRIOR FILING DATE: 1999-01-26
  28  <160> NUMBER OF SEQ ID NOS: 39
  30  <170> SOFTWARE: PatentIn Ver. 2.1
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ERRORED SEQUENCES

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     241  <210> SEQ ID NO: 7
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     243  <212> TYPE: DNA
     244  <213> ORGANISM: ARTHROBACTER sp.S34
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E-->  247  cccgccagta cctaccgcct tcagatctcg gcggagttca ccctcttcga cgcggcgcgc
     248  60
E-->  249  atcgtgccct acctgcaccg cctcggcgcc gactggctgt acctctcgcc gctgctcgag
     250  120
E-->  251  tccgagtcgg gctcctcgca cggctacgac gtggtcgacc actcccgcgt cgacgccgcc
     252  180
E-->  253  cgcggcgggc cggaggggct cgccgagctc tcccgtgcgg cgcacgagcg cggcatgggc
     254  240
E-->  255  gtcgtcgtcg acatcgtgcc caaccacgtc ggcgtcgcga cgccgaaggc gaaccgctgg
     256  300
E-->  257  tggtgggacg ttctggcccg tggacagcgg tcggagtacg ccgactactt cgacatcgac
     258  360
E-->  259  tgggagttcg gcggcggcag gctgcgcctg cccgtgctcg gcgacggccc cgacgagctc
     260  420
E-->  261  gacgcgctga gagtggatgg cgacgagctc gtctactacg agcaccgctt cccgatcgcc
     262  480
E-->  263  gagggcaccg gcggcggcac cccgcgcgag gtgcacgacc ggcagcacta cgagctgatg
     264  540
E-->  265  tcgtggcggc gggccgacca cgacctcaac taccgccgct tcttcgccgt gaacacgctc
```

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        266 600
E--> 267 gccgccgtac gcgtcgaaga cccgcgcgtg ttcgacgaca cccaccgcga gatcggccgc
        268 660
E--> 269 tggatcgccg agggcctcgt cgacggcctg cgcgtcgacc accccgacgg gctgcgcgcc
        270 720
E--> 271 cccggcgact acctgcgccg tctcgccgag ctcgcccaag gcaggccgat ctgggtcgag
        272 780
E--> 273 aagatcatcg agggcgacga gcggatgccc ccgcagtggc ccatcgccgg caccaccggc
        274 840
E--> 275 tacgacgcgc tggccgggat cgaccgggtg ctcgtcgacc ccgcgggcga gcatccgctc
        276 900
E--> 277 acccagatcg tcgacgaggc ggcaggcagc ccccggcgct gggccgagct ggttcccgag
        278 960
E--> 279 cgcaagcggg ccgtcgcccg cggcatcctg aactccgaga tccgccgcgt cgcccgcgaa
        280 1020
E--> 281 ctcggagagg tcgccggcga cgtcgaagac gcgctcgtcg agatcgccgc cgccctgtcc
        282 1080
E--> 283 gtctaccgca gctacctgcc gttcgggcgc gagcacctcg acgaagccgt ggccgccgcg
        284 1140
E--> 285 caggccgcag cccccagct cgaggccgac ctcgccgccg tcggcgcagc gctcgccgac
        286 1200
E--> 287 ccgggcaacc ccgccgcgct ccgcttccag cagaccagcg gcatgatcat ggccaagggc
        288 1260
E--> 289 gtcgaggaca acgcgttcta ccgctacccc cggctcacct cgctgaccga ggtcggggga
        290 1320
E--> 291 gacccgagcc tgttcgcgat cgacgcggcc gccttccacg cggcgcagcg cgaccgcgcc
        292 1380
E--> 293 gcccggctgc ccgagtcgat gacgacgctg accacccacg acaccaagcg cagcgaagac
        294 1440
E--> 295 acccgggcgc ggatcaccgc gctcgccgag gcccccgaac gctggcggcg cttcctgacc
        296 1500
E--> 297 gaggtcggcg ggctcatcgg aacgggcgac cgggtgctgg agaacctgat ctggcaggcg
        298 1560
E--> 299 atcgtcggcg cgtggccggc gagccgggag cggctcgagg cctacgcgct gaaggccgcg
        300 1620
E--> 301 cgcgaagccg gcgagtcgac cgactggatc gacggcgacc ccgcgttcga agagcggctg
        302 1680
E--> 303 acccgcctgg tcacggtcgc cgtcgaggag ccgctcgtgc acgagctgct cgagcggctc
        304 1740
E--> 305 gtcgacgagc tgacggcggc cgggtactcc aacggcctcg cggcgaagct gctgcagctg
        306 1800
E--> 307 ctcgcccccg gaacccccga cgtgtaccag ggcacggaac gctgggaccg gtcgctggtg
        308 1860
E--> 309 gacccggaca accgtcgccc cgtggatttc gccgcggcat ccgagctgct cgaccgcctc
        310 1920
E--> 311 gacggcggct ggcggccgcc cgtcgacgag accggcgcgg tcaagacgct cgtcgtctcc
        312 1980
E--> 313 cgcgcgctgc ggctgcgccg cgaccggccc gagctgttca ccgcgtacca cccggtcacg
        314 2040
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E--> 315 gcgcgcggcg cgcaggccga gcacctgatc ggcttcgacc gcggcggcgc gatcgccctg
     316 2100
E--> 317 gccacccgcc tgccgctcgg cctcgccgcc gcaggcggct ggggcgacac ggtcgtcgac
     318 2160
E--> 319 gtcggcgagc ggagcctgcg cgacgagctg accggccgcg aggcccgcgg agcggcgcgc
     320 2220
E--> 321 gtggccgagt tgttcgccga ctaccccgtc gccctgctgg tggagaca
     322 2268
     325 <210> SEQ ID NO: 8
     326 <211> LENGTH: 28
     327 <212> TYPE: DNA
     328 <213> ORGANISM: ARTHROBACTER sp.S34
     330 <400> SEQUENCE: 8
E--> 331 tttttaata aaatcaggag gaaaaaat
     332 28
     529 <210> SEQ ID NO: 17
     530 <211> LENGTH: 1725
     531 <212> TYPE: DNA
     532 <213> ORGANISM: ARTHROBACTER sp.S34
     534 <400> SEQUENCE: 17
E--> 535 atgaaccgac gattcccggt ctgggcgccc caggccgcgc aggtgacgct cgtcgtgggc
     536 60
E--> 537 caaggccgcg ccgaactccc gctgacccgc gacgagaacg gatggtgggc tcttcagcag
     538 120
E--> 539 ccgtgggacg gcggccccga cctcgtcgac tacggctacc tcgtcgacgg caagggcccc
     540 180
E--> 541 ttcgccgacc cgcggtcgct gcggcagccg cgcggcgtgc acgagctcgg ccgcgaattc
     542 240
E--> 543 gaccccgccc gctacgcgtg gggcgacgac ggatggcgcg gccgagacct caccggagcc
     544 300
E--> 545 gtgatctacg aactgcacgt cggcaccttc acccctgagg gaacgctgga cagcgccatc
     546 360
E--> 547 cgtcgcctcg accacctggt gcgcctcggc gtcgacgcg tcgagctgct gcccgtcaac
     548 420
E--> 549 gcgttcaacg gcacccacgg ctggggctac gacggggtgc tctggtacgc ggtgcacgag
     550 480
E--> 551 ccctacggcg gcccggaggc gtaccagcgc ttcgtcgacg cctgccacgc ccgcggcctc
     552 540
E--> 553 gccgtcgtgc aggacgtcgt ctacaaccac ctgggcccga gcggcaacca cctgcccgac
     554 600
E--> 555 ttcggcccct acctcgggtc gggcgccgcc aacacctggg gcgacgcgct gaacctcgac
     556 660
E--> 557 gggccgctct ccgacgaggt gcggcggtac atcatcgaca acgcggtgta ctggctgcgc
     558 720
E--> 559 gacatgcacg ccgacgggct gcggctcgac gccgtgcacg cgctgcgcga cgcccgcgcg
     560 780
E--> 561 ctgcacctgc tcgaagagct cgccgcccgc gtcgacgagc tggcgggcga gctcggccgg
     562 840
E--> 563 ccgctgacgc tcatcgccga gagcgacctg aacgacccga agctgatccg ctcccgcgcg
```

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```
        564 900
E--> 565 gcgcacggct acggcctcga cgcccagtgg gacgacgacg tgcaccacgc ggtgcacgcc
        566 960
E--> 567 aacgtgaccg gcgagaccgt cggctactac gccgacttcg gcgggctcgg cgccctcgtc
        568 1020
E--> 569 aaggtgttcc agcgcggctg gttccacgac ggcacctggt cgagcttccg cgagcggcac
        570 1080
E--> 571 cacggccggc cgctcgaccc cgacatcccg ttccgccggc tcgtcgcctt cgcgcaggat
        572 1140
E--> 573 cacgaccagg tcggcaaccg agcggtcggc gaccgcatgt cggcgcaggt cggcgagggt
        574 1200
E--> 575 tcgctcgccg ccgcggcggc gctcgtgctg ctcggcccgt tcaccccgat gctgttcatg
        576 1260
E--> 577 ggcgaggagt ggggcgcgcg cacccgtgg cagttcttca cctcccaccc cgagcccgag
        578 1320
E--> 579 ctgggggagg cgacggcgcg cgggcgcatc gccgagttcg cccgcatggg ctgggacccg
        580 1380
E--> 581 gcagtcgtgc ccgacccgca ggacccggcc accttcgccc gctcgcacct ggactggtcc
        582 1440
E--> 583 gagcccgagc gggaaccgca cgcgggcctg ctcgccttct acaccgacct gatcgcgctg
        584 1500
E--> 585 cggcgcgagc tgccggtcga tgcgccggcg cgcgaggtgg atgccgacga ggcgcgcggc
        586 1560
E--> 587 gtcttcgcgt tcagccgcgg cccgctgcgg gtcacggtcg cgctgcgccc cggaccggtc
        588 1620
E--> 589 ggggtgcccg agcacggggg cctcgtgctc gcctacggcg aggtgcgcgc cggcgccgcc
        590 1680
E--> 591 ggactgcacc tcgacgggcc gggagccgcg atcgtgcgcc tcgag
        592 1725
        595 <210> SEQ ID NO: 18
        596 <211> LENGTH: 23
        597 <212> TYPE: DNA
        598 <213> ORGANISM: ARTHROBACTER sp.S34
        600 <400> SEQUENCE: 18
E--> 601 gcsaaccgst ggtggtggga cgt
        602 23
        605 <210> SEQ ID NO: 19
        606 <211> LENGTH: 3252
        607 <212> TYPE: DNA
        608 <213> ORGANISM: ARTHROBACTER sp.S34
        610 <220> FEATURE:
        611 <221> NAME/KEY: 5'UTR
        612 <222> LOCATION: (1)..(742)
        614 <220> FEATURE:
        615 <221> NAME/KEY: CDS
        616 <222> LOCATION: (743)..(3013)
        618 <220> FEATURE:
        619 <221> NAME/KEY: 3'UTR
        620 <222> LOCATION: (742)..(3014)
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done

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      622 <400> SEQUENCE: 19
E--> 623 atgccgacga cgaacttgag cgcgttctcg ggcacccgcg agagcggtcc gcgcacggcg
     624 60
E--> 626 gcgcccagtg ccacgacgag cacgatcgcg gcgagcgccg cgacgacggc gaccggcagg
     627 120
E--> 629 cgccctgat tgctggcgaa ggtgagcacg atgaagacca cctcgaggcc ctcgagcaac
     630 180
E--> 632 acacctttga acgacacggt gaacgcgtac caatcggaga ccccgaaccg gctctcgcgc
     633 240
E--> 635 cgggcgctct cggccgcctc gacctgacgc cggaaggcag cctcctcgtc acggagagcc
     636 300
E--> 638 ctgcgccctg ccgcgcgcag caccgccttg cgcagccagc cgagcccgaa gacgagcagc
     639 360
E--> 641 aacccgccga cgacgaggcg cagcacggcc agcggcagca gcaggatcgc gggaccgacg
     642 420
E--> 644 agcgcgacgg ccgcggccag caccaccacg gcgacgcgg cacctgtcag cgccgaccgc
     645 480
E--> 647 cagctgcggg tggcgccgac cgcgacgacg atcgtggtcg cctccaccgc ctcgaccacg
     648 540
E--> 650 caggcgagga acacggcggc gaacagggcg acggcggtca tcggcccagc agacggttga
     651 600
E--> 653 ccatcacggc acgctagcgc cattgctcac aggaagggcc aagacgcccg caacgcggca
     654 660
E--> 656 cccgtggacg gcgcgtaccg gcgtgtgacc gatcgtgtca accggtggcg cccgccccga
     657 720
E--> 659 gcacctgcgt agattcggcc tc gtg ccc gcc agt acc tac cgc ctt cag atc
     660 772
     661                        Met Pro Ala Ser Thr Tyr Arg Leu Gln Ile
     662                         1               5                   10
E--> 664 tcg gcg gag ttc acc ctc ttc gac gcg gcg cgc atc gtg ccc tac ctg
     665 820
     666 Ser Ala Glu Phe Thr Leu Phe Asp Ala Ala Arg Ile Val Pro Tyr Leu
     667                  15                  20                  25
E--> 669 cac cgc ctc ggc gcc gac tgg ctg tac ctc tcg ccg ctg ctc gag tcc
     670 868
     671 His Arg Leu Gly Ala Asp Trp Leu Tyr Leu Ser Pro Leu Leu Glu Ser
     672               30                  35                  40
E--> 674 gag tcg ggc tcc tcg cac ggc tac gac gtg gtc gac cac tcc cgc gtc
     675 916
     676 Glu Ser Gly Ser Ser His Gly Tyr Asp Val Val Asp His Ser Arg Val
     677               45                  50                  55
E--> 679 gac gcc gcc cgc ggc ggg ccg gag ggg ctc gcc gag ctc tcc cgt gcg
     680 964
     681 Asp Ala Ala Arg Gly Gly Pro Glu Gly Leu Ala Glu Leu Ser Arg Ala
     682       60                  65                  70
E--> 684 gcg cac gag cgc ggc atg ggc gtc gtc gtc gac atc gtg ccc aac cac
     685 1012
     686 Ala His Glu Arg Gly Met Gly Val Val Val Asp Ile Val Pro Asn His
     687 75                  80                  85                  90
```

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                    Input Set : A:\Yamamto1.app
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E--> 689 gtc ggc gtc gcg acg ccg aag gcg aac cgc tgg tgg tgg gac gtt ctg
     690 1060
     691 Val Gly Val Ala Thr Pro Lys Ala Asn Arg Trp Trp Trp Asp Val Leu
     692                      95              100              105
E--> 694 gcc cgt gga cag cgg tcg gag tac gcc gac tac ttc gac atc gac tgg
     695 1108
     696 Ala Arg Gly Gln Arg Ser Glu Tyr Ala Asp Tyr Phe Asp Ile Asp Trp
     697              110              115              120
E--> 699 gag ttc ggc ggc ggc agg ctg cgc ctg ccc gtg ctc ggc gac ggc ccc
     700 1156
     701 Glu Phe Gly Gly Gly Arg Leu Arg Leu Pro Val Leu Gly Asp Gly Pro
     702          125              130              135
E--> 704 gac gag ctc gac gcg ctg aga gtg gat ggc gac gag ctc gtc tac tac
     705 1204
     706 Asp Glu Leu Asp Ala Leu Arg Val Asp Gly Asp Glu Leu Val Tyr Tyr
     707      140              145              150
E--> 709 gag cac cgc ttc ccg atc gcc gag ggc acc ggc ggc ggc acc ccg cgc
     710 1252
     711 Glu His Arg Phe Pro Ile Ala Glu Gly Thr Gly Gly Gly Thr Pro Arg
     712 155              160              165              170
E--> 714 gag gtg cac gac cgg cag cac tac gag ctg atg tcg tgg cgg cgg gcc
     715 1300
     716 Glu Val His Asp Arg Gln His Tyr Glu Leu Met Ser Trp Arg Arg Ala
     717              175              180              185
E--> 719 gac cac gac ctc aac tac cgc cgc ttc ttc gcc gtg aac acg ctc gcc
     720 1348
     721 Asp His Asp Leu Asn Tyr Arg Arg Phe Phe Ala Val Asn Thr Leu Ala
     722              190              195              200
E--> 724 gcc gta cgc gtc gaa gac ccg cgc gtg ttc gac gac acc cac cgc gag
     725 1396
     726 Ala Val Arg Val Glu Asp Pro Arg Val Phe Asp Asp Thr His Arg Glu
     727          205              210              215
E--> 729 atc ggc cgc tgg atc gcc gag ggc ctc gtc gac ggc ctg cgc gtc gac
     730 1444
     731 Ile Gly Arg Trp Ile Ala Glu Gly Leu Val Asp Gly Leu Arg Val Asp
     732      220              225              230
E--> 734 cac ccc gac ggg ctg cgc gcc ccc ggc gac tac ctg cgc cgt ctc gcc
     735 1492
     736 His Pro Asp Gly Leu Arg Ala Pro Gly Asp Tyr Leu Arg Arg Leu Ala
     737 235              240              245              250
E--> 739 gag ctc gcc caa ggc agg ccg atc tgg gtc gag aag atc atc gag ggc
     740 1540
     741 Glu Leu Ala Gln Gly Arg Pro Ile Trp Val Glu Lys Ile Ile Glu Gly
     742              255              260              265
E--> 744 gac gag cgg atg ccc ccg cag tgg ccc atc gcc ggc acc acc ggc tac
     745 1588
     746 Asp Glu Arg Met Pro Pro Gln Trp Pro Ile Ala Gly Thr Thr Gly Tyr
     747              270              275              280
E--> 749 gac gcg ctg gcc ggg atc gac cgg gtg ctc gtc gac ccc gcg ggc gag
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      750 1636
      751 Asp Ala Leu Ala Gly Ile Asp Arg Val Leu Val Asp Pro Ala Gly Glu
      752         285             290             295
E--> 754 cat ccg ctc acc cag atc gtc gac gag gcg gca ggc agc ccc cgg cgc
      755 1684
      756 His Pro Leu Thr Gln Ile Val Asp Glu Ala Ala Gly Ser Pro Arg Arg
      757         300             305             310
E--> 759 tgg gcc gag ctg gtt ccc gag cgc aag cgg gcc gtc gcc cgc ggc atc
      760 1732
      761 Trp Ala Glu Leu Val Pro Glu Arg Lys Arg Ala Val Ala Arg Gly Ile
      762 315             320             325             330
E--> 764 ctg aac tcc gag atc cgc cgc gtc gcc cgc gaa ctc gga gag gtc gcc
      765 1780
      766 Leu Asn Ser Glu Ile Arg Arg Val Ala Arg Glu Leu Gly Glu Val Ala
      767             335             340             345
E--> 769 ggc gac gtc gaa gac gcg ctc gtc gag atc gcc gcc gcc ctg tcc gtc
      770 1828
      771 Gly Asp Val Glu Asp Ala Leu Val Glu Ile Ala Ala Ala Leu Ser Val
      772         350             355             360
E--> 774 tac cgc agc tac ctg ccg ttc ggg cgc gag cac ctc gac gaa gcc gtg
      775 1876
      776 Tyr Arg Ser Tyr Leu Pro Phe Gly Arg Glu His Leu Asp Glu Ala Val
      777         365             370             375
E--> 779 gcc gcc gcg cag gcc gca gcc ccc cag ctc gag gcc gac ctc gcc gcc
      780 1924
      781 Ala Ala Ala Gln Ala Ala Ala Pro Gln Leu Glu Ala Asp Leu Ala Ala
      782         380             385             390
E--> 784 gtc ggc gca gcg ctc gcc gac ccg ggc aac ccc gcc gcg ctc cgc ttc
      785 1972
      786 Val Gly Ala Ala Leu Ala Asp Pro Gly Asn Pro Ala Ala Leu Arg Phe
      787 395             400             405             410
E--> 789 cag cag acc agc ggc atg atc atg gcc aag ggc gtc gag gac aac gcg
      790 2020
      791 Gln Gln Thr Ser Gly Met Ile Met Ala Lys Gly Val Glu Asp Asn Ala
      792             415             420             425
E--> 794 ttc tac cgc tac ccc cgg ctc acc tcg ctg acc gag gtc ggg gga gac
      795 2068
      796 Phe Tyr Arg Tyr Pro Arg Leu Thr Ser Leu Thr Glu Val Gly Gly Asp
      797         430             435             440
E--> 799 ccg agc ctg ttc gcg atc gac gcg gcc gcc ttc cac gcg gcg cag cgc
      800 2116
      801 Pro Ser Leu Phe Ala Ile Asp Ala Ala Ala Phe His Ala Ala Gln Arg
      802         445             450             455
E--> 804 gac cgc gcc gcc cgg ctg ccc gag tcg atg acg acg ctg acc acc cac
      805 2164
      806 Asp Arg Ala Ala Arg Leu Pro Glu Ser Met Thr Thr Leu Thr Thr His
      807         460             465             470
E--> 809 gac acc aag cgc agc gaa gac acc cgg gcg cgg atc acc gcg ctc gcc
      810 2212
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```
      811 Asp Thr Lys Arg Ser Glu Asp Thr Arg Ala Arg Ile Thr Ala Leu Ala
      812 475                 480                 485                 490
E--> 814 gag gcc ccc gaa cgc tgg cgg cgc ttc ctg acc gag gtc ggc ggg ctc
      815 2260
      816 Glu Ala Pro Glu Arg Trp Arg Arg Phe Leu Thr Glu Val Gly Gly Leu
      817             495                 500                 505
E--> 819 atc gga acg ggc gac cgg gtg ctg gag aac ctg atc tgg cag gcg atc
      820 2308
      821 Ile Gly Thr Gly Asp Arg Val Leu Glu Asn Leu Ile Trp Gln Ala Ile
      822             510                 515                 520
E--> 824 gtc ggc gcg tgg ccg gcg agc cgg gag cgg ctc gag gcc tac gcg ctg
      825 2356
      826 Val Gly Ala Trp Pro Ala Ser Arg Glu Arg Leu Glu Ala Tyr Ala Leu
      827             525                 530                 535
E--> 829 aag gcc gcg cgc gaa gcc ggc gag tcg acc gac tgg atc gac ggc gac
      830 2404
      831 Lys Ala Ala Arg Glu Ala Gly Glu Ser Thr Asp Trp Ile Asp Gly Asp
      832         540                 545                 550
E--> 834 ccc gcg ttc gaa gag cgg ctg acc cgc ctg gtc acg gtc gcc gtc gag
      835 2452
      836 Pro Ala Phe Glu Glu Arg Leu Thr Arg Leu Val Thr Val Ala Val Glu
      837 555                 560                 565                 570
E--> 839 gag ccg ctc gtg cac gag ctg ctc gag cgg ctc gtc gac gag ctg acg
      840 2500
      841 Glu Pro Leu Val His Glu Leu Leu Glu Arg Leu Val Asp Glu Leu Thr
      842             575                 580                 585
E--> 844 gcg gcc ggg tac tcc aac ggc ctc gcg gcg aag ctg ctg cag ctg ctc
      845 2548
      846 Ala Ala Gly Tyr Ser Asn Gly Leu Ala Ala Lys Leu Leu Gln Leu Leu
      847             590                 595                 600
E--> 849 gcc ccc gga acc ccc gac gtg tac cag ggc acg gaa cgc tgg gac cgg
      850 2596
      851 Ala Pro Gly Thr Pro Asp Val Tyr Gln Gly Thr Glu Arg Trp Asp Arg
      852         605                 610                 615
E--> 854 tcg ctg gtg gac ccg gac aac cgt cgc ccc gtg gat ttc gcc gcg gca
      855 2644
      856 Ser Leu Val Asp Pro Asp Asn Arg Arg Pro Val Asp Phe Ala Ala Ala
      857     620                 625                 630
E--> 859 tcc gag ctg ctc gac cgc ctc gac ggc ggc tgg cgg ccg ccc gtc gac
      860 2692
      861 Ser Glu Leu Leu Asp Arg Leu Asp Gly Gly Trp Arg Pro Pro Val Asp
      862 635                 640                 645                 650
E--> 864 gag acc ggc gcg gtc aag acg ctc gtc gtc tcc cgc gcg ctg cgg ctg
      865 2740
      866 Glu Thr Gly Ala Val Lys Thr Leu Val Val Ser Arg Ala Leu Arg Leu
      867             655                 660                 665
E--> 869 cgc cgc gac cgg ccc gag ctg ttc acc gcg tac cac ccg gtc acg gcg
      870 2788
      871 Arg Arg Asp Arg Pro Glu Leu Phe Thr Ala Tyr His Pro Val Thr Ala
```

Bame (signature)

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                  RAW SEQUENCE LISTING                DATE: 03/23/2001
                  PATENT APPLICATION:  US/09/435,770  TIME: 16:39:39

                  Input Set : A:\Yamamtol.app
                  Output Set: N:\CRF3\03232001\I435770.raw

        872           670              675              680
E--> 874 cgc ggc gcg cag gcc gag cac ctg atc ggc ttc gac cgc ggc ggc gcg
     875 2836
     876 Arg Gly Ala Gln Ala Glu His Leu Ile Gly Phe Asp Arg Gly Gly Ala
     877           685              690              695
E--> 879 atc gcc ctg gcc acc cgc ctg ccg ctc ggc ctc gcc gcc gca ggc ggc
     880 2884
     881 Ile Ala Leu Ala Thr Arg Leu Pro Leu Gly Leu Ala Ala Ala Gly Gly
     882       700              705              710
E--> 884 tgg ggc gac acg gtc gtc gac gtc ggc gag cgg agc ctg cgc gac gag
     885 2932
     886 Trp Gly Asp Thr Val Val Asp Val Gly Glu Arg Ser Leu Arg Asp Glu
     887 715              720              725              730
E--> 889 ctg acc ggc cgc gag gcc cgc gga gcg gcg cgc gtg gcc gag ttg ttc
     890 2980
     891 Leu Thr Gly Arg Glu Ala Arg Gly Ala Ala Arg Val Ala Glu Leu Phe
     892               735              740              745
E--> 894 gcc gac tac ccc gtc gcc ctg ctg gtg gag aca tgaaccgacg attcccggtc
     895 3033
     896 Ala Asp Tyr Pro Val Ala Leu Leu Val Glu Thr
     897               750              755
E--> 899 tgggcgcccc aggccgcgca ggtgacgctc gtcgtgggcc aaggccgcgc cgaactcccg
     900 3093
E--> 902 ctgacccgcg acgagaacgg atggtgggct cttcagcagc cgtgggacgg cggccccgac
     903 3153
E--> 905 ctcgtcgact acggctacct cgtcgacggc aagggcccct tcgccgaccc gcggtcgctg
     906 3213
E--> 908 cggcagccgc gcggcgtgca cgagctcggc cgcgaattc
     909 3252
     913 <210> SEQ ID NO: 20
     914 <211> LENGTH: 26
     915 <212> TYPE: DNA
     916 <213> ORGANISM: Artificial Sequence
     918 <220> FEATURE:
     919 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
     921 <400> SEQUENCE: 20
E--> 922 atgcccgcca gtacctaccg ccttca
     923 26
     926 <210> SEQ ID NO: 21
     927 <211> LENGTH: 25
     928 <212> TYPE: DNA
     929 <213> ORGANISM: Artificial Sequence
     931 <220> FEATURE:
     932 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
     934 <400> SEQUENCE: 21
E--> 935 tcatgtctcc accagcaggg cgacg
     936 25
     939 <210> SEQ ID NO: 22
     940 <211> LENGTH: 50
```

```
                    RAW SEQUENCE LISTING              DATE: 03/23/2001
                    PATENT APPLICATION:  US/09/435,770    TIME: 16:39:39

                    Input Set : A:\Yamamtol.app
                    Output Set: N:\CRF3\03232001\I435770.raw

       941 <212> TYPE: DNA
       942 <213> ORGANISM: Artificial Sequence
       944 <220> FEATURE:
       945 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
       947 <400> SEQUENCE: 22
E--> 948 aattcttttt taataaaatc aggaggaatc tagatgttta ctagtctgca
       949 50
       952 <210> SEQ ID NO: 23
       953 <211> LENGTH: 42
       954 <212> TYPE: DNA
       955 <213> ORGANISM: Artificial Sequence
       957 <220> FEATURE:
       958 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
       960 <400> SEQUENCE: 23
E--> 961 gactagtaaa catctagatt cctcctgatt ttattaaaaa ag
       962 42
       965 <210> SEQ ID NO: 24
       966 <211> LENGTH: 33
       967 <212> TYPE: DNA
       968 <213> ORGANISM: Artificial Sequence
       970 <220> FEATURE:
       971 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
       973 <400> SEQUENCE: 24
E--> 974 aaatctagat gcccgccagt acctaccgcc ttc
       975 33
       978 <210> SEQ ID NO: 25
       979 <211> LENGTH: 33
       980 <212> TYPE: DNA
       981 <213> ORGANISM: Artificial Sequence
       983 <220> FEATURE:
       984 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
       986 <400> SEQUENCE: 25
E--> 987 aaaactagtt tatcatgtct ccaccagcag ggc
       988 33
       991 <210> SEQ ID NO: 26
       992 <211> LENGTH: 22
       993 <212> TYPE: DNA
       994 <213> ORGANISM: Artificial Sequence
       996 <220> FEATURE:
       997 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
       999 <400> SEQUENCE: 26
E--> 1000 atcggtgatg tcggcgatat ag
      1001 22
      1004 <210> SEQ ID NO: 27
      1005 <211> LENGTH: 29
      1006 <212> TYPE: DNA
      1007 <213> ORGANISM: Artificial Sequence
      1009 <220> FEATURE:
      1010 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
```

same

```
                    RAW SEQUENCE LISTING              DATE: 03/23/2001
                    PATENT APPLICATION:  US/09/435,770  TIME: 16:39:39

                    Input Set : A:\Yamamtol.app
                    Output Set: N:\CRF3\03232001\I435770.raw

          1012 <400> SEQUENCE: 27
E--> 1013 gtactggcgg gcatattttt tcctcctga
          1014 29
          1017 <210> SEQ ID NO: 28
          1018 <211> LENGTH: 31
          1019 <212> TYPE: DNA
          1020 <213> ORGANISM: Artificial Sequence
          1022 <220> FEATURE:
          1023 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
          1025 <400> SEQUENCE: 28
E--> 1026 aatcaggagg aaaaaatatg cccgccagta c
          1027 31
          1030 <210> SEQ ID NO: 29
          1031 <211> LENGTH: 22
          1032 <212> TYPE: DNA
          1033 <213> ORGANISM: Artificial Sequence
          1035 <220> FEATURE:
          1036 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
          1038 <400> SEQUENCE: 29
E--> 1039 tcgacgatct gggtgagcgg at
          1040 22
          1043 <210> SEQ ID NO: 30
          1044 <211> LENGTH: 22
          1045 <212> TYPE: DNA
          1046 <213> ORGANISM: Artificial Sequence
          1048 <220> FEATURE:
          1049 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
          1051 <400> SEQUENCE: 30
E--> 1052 tcgacgagca cccggtcgat cc
          1053 22
          1056 <210> SEQ ID NO: 31
          1057 <211> LENGTH: 26
          1058 <212> TYPE: DNA
          1059 <213> ORGANISM: Artificial Sequence
          1061 <220> FEATURE:
          1062 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
          1064 <400> SEQUENCE: 31
E--> 1065 cartgggayg aygaygtnga ycaygc
          1066 26
          1069 <210> SEQ ID NO: 32
          1070 <211> LENGTH: 2218
          1071 <212> TYPE: DNA
          1072 <213> ORGANISM: Artificial Sequence
          1074 <220> FEATURE:
          1075 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
          1077 <220> FEATURE:
          1078 <221> NAME/KEY: CDS
          1079 <222> LOCATION: (477)..(2201)
          1081 <220> FEATURE:
```

same

→ *see item 10 on Erra Summary sheet*

```
        1082  <221> NAME/KEY: 3'UTR
        1083  <222> LOCATION: (2202)..(2218)
E-->    1085  <400> SEQUENCE: 33   32  ← change to 32
E-->    1086  ctgcagctgc tcgcccccgg aaccccgac gtgtaccagg gcacggaacg ctgggaccgg
        1087  60
E-->    1089  tcgctggtgg acccggacaa ccgtcgcccc gtggatttcg ccgcggcatc cgagctgctc
        1090  120
E-->    1092  gaccgcctcg acggcggctg gcggccgccc gtcgacgaga ccggcgcggt caagacgctc
        1093  180
E-->    1095  gtcgtctccc gcgcgctgcg gctgcgccgc gaccggcccg agctgttcac cgcgtaccac
        1096  240
E-->    1098  ccggtcacgg cgcgcggcgc gcaggccgag cacctgatcg gcttcgaccg cggcggcgcg
        1099  300
E-->    1101  atcgccctgg ccacccgcct gccgctcggc ctcgccgccg caggcggctg gggcgacacg
        1102  360
E-->    1104  gtcgtcgacg tcggcgagcg gagcctgcgc gacgagctga ccggccgcga ggcccgcgga
        1105  420
E-->    1107  gcggcgcgcg tggccgagtt gttcgccgac taccccgtcg ccctgctggt ggagac atg
        1108  479
        1109                                                          Met
        1110                                                            1
E-->    1112  aac cga cga ttc ccg gtc tgg gcg ccc cag gcc gcg cag gtg acg ctc
        1113  527
        1114  Asn Arg Arg Phe Pro Val Trp Ala Pro Gln Ala Ala Gln Val Thr Leu
        1115              5               10              15
E-->    1117  gtc gtg ggc caa ggc cgc gcc gaa ctc ccg ctg acc cgc gac gag aac
        1118  575
        1119  Val Val Gly Gln Gly Arg Ala Glu Leu Pro Leu Thr Arg Asp Glu Asn
        1120              20              25              30
E-->    1122  gga tgg tgg gct ctt cag cag ccg tgg gac ggc ggc ccc gac ctc gtc
        1123  623
        1124  Gly Trp Trp Ala Leu Gln Gln Pro Trp Asp Gly Gly Pro Asp Leu Val
        1125          35              40              45
E-->    1127  gac tac ggc tac ctc gtc gac ggc aag ggc ccc ttc gcc gac ccg cgg
        1128  671
        1129  Asp Tyr Gly Tyr Leu Val Asp Gly Lys Gly Pro Phe Ala Asp Pro Arg
        1130  50              55              60              65
E-->    1132  tcg ctg cgg cag ccg cgc ggc gtg cac gag ctc ggc cgc gaa ttc gac
        1133  719
        1134  Ser Leu Arg Gln Pro Arg Gly Val His Glu Leu Gly Arg Glu Phe Asp
        1135              70              75              80
E-->    1137  ccc gcc cgc tac gcg tgg ggc gac gac gga tgg cgc ggc cga gac ctc
        1138  767
        1139  Pro Ala Arg Tyr Ala Trp Gly Asp Asp Gly Trp Arg Gly Arg Asp Leu
        1140              85              90              95
E-->    1142  acc gga gcc gtg atc tac gaa ctg cac gtc ggc acc ttc acc cct gag
        1143  815
        1144  Thr Gly Ala Val Ile Tyr Glu Leu His Val Gly Thr Phe Thr Pro Glu
        1145              100             105             110
```

same format err

RAW SEQUENCE LISTING   DATE: 03/23/2001
PATENT APPLICATION: US/09/435,770   TIME: 16:39:39

Input Set : A:\Yamamto1.app
Output Set: N:\CRF3\03232001\I435770.raw

```
E--> 1147 gga acg ctg gac agc gcc atc cgt cgc ctc gac cac ctg gtg cgc ctc
     1148 863
     1149 Gly Thr Leu Asp Ser Ala Ile Arg Arg Leu Asp His Leu Val Arg Leu
     1150     115             120             125
E--> 1152 ggc gtc gac gcg gtc gag ctg ctg ccc gtc aac gcg ttc aac ggc acc
     1153 911
     1154 Gly Val Asp Ala Val Glu Leu Leu Pro Val Asn Ala Phe Asn Gly Thr
     1155 130             135             140             145
E--> 1157 cac ggc tgg ggc tac gac ggg gtg ctc tgg tac gcg gtg cac gag ccc
     1158 959
     1159 His Gly Trp Gly Tyr Asp Gly Val Leu Trp Tyr Ala Val His Glu Pro
     1160             150             155  ·          160
E--> 1162 tac ggc ggc ccg gag gcg tac cag cgc ttc gtc gac gcc tgc cac gcc
     1163 1007
     1164 Tyr Gly Gly Pro Glu Ala Tyr Gln Arg Phe Val Asp Ala Cys His Ala
     1165             165             170             175
E--> 1167 cgc ggc ctc gcc gtc gtg cag gac gtc gtc tac aac cac ctg ggc ccg
     1168 1055
     1169 Arg Gly Leu Ala Val Val Gln Asp Val Val Tyr Asn His Leu Gly Pro
     1170             180             185             190
E--> 1172 agc ggc aac cac ctg ccc gac ttc ggc ccc tac ctc ggg tcg ggc gcc
     1173 1103
     1174 Ser Gly Asn His Leu Pro Asp Phe Gly Pro Tyr Leu Gly Ser Gly Ala
     1175     195             200             205
E--> 1177 gcc aac acc tgg ggc gac gcg ctg aac ctc gac ggg ccg ctc tcc gac
     1178 1151
     1179 Ala Asn Thr Trp Gly Asp Ala Leu Asn Leu Asp Gly Pro Leu Ser Asp
     1180 210             215             220             225
E--> 1182 gag gtg cgg cgg tac atc atc gac aac gcg gtg tac tgg ctg cgc gac
     1183 1199
     1184 Glu Val Arg Arg Tyr Ile Ile Asp Asn Ala Val Tyr Trp Leu Arg Asp
     1185             230             235             240
E--> 1187 atg cac gcc gac ggg ctg cgg ctc gac gcc gtg cac gcg ctg cgc gac
     1188 1247
     1189 Met His Ala Asp Gly Leu Arg Leu Asp Ala Val His Ala Leu Arg Asp
     1190             245             250             255
E--> 1192 gcc cgc gcg ctg cac ctg ctc gaa gag ctc gcc gcc cgc gtc gac gag
     1193 1295
     1194 Ala Arg Ala Leu His Leu Leu Glu Glu Leu Ala Ala Arg Val Asp Glu
     1195             260             265             270
E--> 1197 ctg gcg ggc gag ctc ggc cgg ccg ctg acg ctc atc gcc gag agc gac
     1198 1343
     1199 Leu Ala Gly Glu Leu Gly Arg Pro Leu Thr Leu Ile Ala Glu Ser Asp
     1200     275             280             285
E--> 1202 ctg aac gac ccg aag ctg atc cgc tcc cgc gcg gcg cac ggc tac ggc
     1203 1391
     1204 Leu Asn Asp Pro Lys Leu Ile Arg Ser Arg Ala Ala His Gly Tyr Gly
     1205 290             295             300             305
E--> 1207 ctc gac gcc cag tgg gac gac gac gtg cac cac gcg gtg cac gcc aac
```

RAW SEQUENCE LISTING   DATE: 03/23/2001
PATENT APPLICATION: US/09/435,770   TIME: 16:39:39

Input Set : A:\Yamamtol.app
Output Set: N:\CRF3\03232001\I435770.raw

```
      1208 1439
      1209 Leu Asp Ala Gln Trp Asp Asp Asp Val His His Ala Val His Ala Asn
      1210               310             315             320
E-->  1212 gtg acc ggc gag acc gtc ggc tac tac gcc gac ttc ggc ggg ctc ggc
      1213 1487
      1214 Val Thr Gly Glu Thr Val Gly Tyr Tyr Ala Asp Phe Gly Gly Leu Gly
      1215           325             330             335
E-->  1217 gcc ctc gtc aag gtg ttc cag cgc ggc tgg ttc cac gac ggc acc tgg
      1218 1535
      1219 Ala Leu Val Lys Val Phe Gln Arg Gly Trp Phe His Asp Gly Thr Trp
      1220           340             345             350
E-->  1222 tcg agc ttc cgc gag cgg cac cac ggc cgg ccg ctc gac ccc gac atc
      1223 1583
      1224 Ser Ser Phe Arg Glu Arg His His Gly Arg Pro Leu Asp Pro Asp Ile
      1225       355             360             365
E-->  1227 ccg ttc cgc cgg ctc gtc gcc ttc gcg cag gat cac gac cag gtc ggc
      1228 1631
      1229 Pro Phe Arg Arg Leu Val Ala Phe Ala Gln Asp His Asp Gln Val Gly
      1230 370             375             380             385
E-->  1232 aac cga gcg gtc ggc gac cgc atg tcg gcg cag gtc ggc gag ggt tcg
      1233 1679
      1234 Asn Arg Ala Val Gly Asp Arg Met Ser Ala Gln Val Gly Glu Gly Ser
      1235           390             395             400
E-->  1237 ctc gcc gcc gcg gcg gcg ctc gtg ctg ctc ggc ccg ttc acc ccg atg
      1238 1727
      1239 Leu Ala Ala Ala Ala Ala Leu Val Leu Leu Gly Pro Phe Thr Pro Met
      1240           405             410             415
E-->  1242 ctg ttc atg ggc gag gag tgg ggc gcg cgc acc ccg tgg cag ttc ttc
      1243 1775
      1244 Leu Phe Met Gly Glu Glu Trp Gly Ala Arg Thr Pro Trp Gln Phe Phe
      1245           420             425             430
E-->  1247 acc tcc cac ccc gag ccc gag ctg ggg gag gcg acg gcg cgc ggg cgc
      1248 1823
      1249 Thr Ser His Pro Glu Pro Glu Leu Gly Glu Ala Thr Ala Arg Gly Arg
      1250       435             440             445
E-->  1252 atc gcc gag ttc gcc cgc atg ggc tgg gac ccg gca gtc gtg ccc gac
      1253 1871
      1254 Ile Ala Glu Phe Ala Arg Met Gly Trp Asp Pro Ala Val Val Pro Asp
      1255 450             455             460             465
E-->  1257 ccg cag gac ccg gcc acc ttc gcc cgc tcg cac ctg gac tgg tcc gag
      1258 1919
      1259 Pro Gln Asp Pro Ala Thr Phe Ala Arg Ser His Leu Asp Trp Ser Glu
      1260           470             475             480
E-->  1262 ccc gag cgg gaa ccg cac gcg ggc ctg ctc gcc ttc tac acc gac ctg
      1263 1967
      1264 Pro Glu Arg Glu Pro His Ala Gly Leu Leu Ala Phe Tyr Thr Asp Leu
      1265           485             490             495
E-->  1267 atc gcg ctg cgg cgc gag ctg ccg gtc gat gcg ccg gcg cgc gag gtg
      1268 2015
```

Input Set : A:\Yamamto1.app
Output Set: N:\CRF3\03232001\I435770.raw

```
      1269 Ile Ala Leu Arg Arg Glu Leu Pro Val Asp Ala Pro Ala Arg Glu Val
      1270         500                 505                 510
E--> 1272 gat gcc gac gag gcg cgc ggc gtc ttc gcg ttc agc cgc ggc ccg ctg
      1273 2063
      1274 Asp Ala Asp Glu Ala Arg Gly Val Phe Ala Phe Ser Arg Gly Pro Leu
      1275       515                 520                 525
E--> 1277 cgg gtc acg gtc gcg ctg cgc ccc gga ccg gtc ggg gtg ccc gag cac
      1278 2111
      1279 Arg Val Thr Val Ala Leu Arg Pro Gly Pro Val Gly Val Pro Glu His
      1280 530                 535                 540                 545
E--> 1282 ggg ggc ctc gtg ctc gcc tac ggc gag gtg cgc gcc ggc gcc gcc gga
      1283 2159
      1284 Gly Gly Leu Val Leu Ala Tyr Gly Glu Val Arg Ala Gly Ala Ala Gly
      1285             550                 555                 560
E--> 1287 ctg cac ctc gac ggg ccg gga gcc gcg atc gtg cgc ctc gag
      1288 2201
      1289 Leu His Leu Asp Gly Pro Gly Ala Ala Ile Val Arg Leu Glu
      1290             565                 570                 575
E--> 1292 tgacgcggct gggtacc
      1293 2218
      1296 <210> SEQ ID NO: 33
      1297 <211> LENGTH: 25
      1298 <212> TYPE: DNA
      1299 <213> ORGANISM: Artificial Sequence
      1301 <220> FEATURE:
      1302 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
      1304 <400> SEQUENCE: 33
E--> 1305 atgaaccgac gattcccggt ctggg
      1306 25
      1308 <210> SEQ ID NO: 34
      1309 <211> LENGTH: 25
      1310 <212> TYPE: DNA
      1311 <213> ORGANISM: Artificial Sequence
      1313 <220> FEATURE:
      1314 <223> OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC
      1316 <400> SEQUENCE: 34
E--> 1317 tcactcgagg cgcacgatcg cggct
      1318 25
```

same

```
                    VERIFICATION SUMMARY               DATE: 03/23/2001
                    PATENT APPLICATION:  US/09/435,770  TIME: 16:39:40

                    Input Set : A:\Yamamto1.app
                    Output Set: N:\CRF3\03232001\I435770.raw

L:247 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:7
M:254 Repeated in SeqNo=7
L:331 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:8
L:535 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:17
M:254 Repeated in SeqNo=17
L:601 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:23 SEQ:18
L:623 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:19
M:254 Repeated in SeqNo=19
L:922 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:20
L:935 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:21
L:948 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:22
L:961 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:42 SEQ:23
L:974 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:24
L:987 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:33 SEQ:25
L:1000 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:26
L:1013 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:27
L:1026 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:31 SEQ:28
L:1039 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:29
L:1052 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:30
L:1065 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1065 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1065 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
L:1065 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:31
L:1085 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32 differs:33
L:1086 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:32
M:254 Repeated in SeqNo=32
L:1305 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:33
L:1317 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:25 SEQ:34
L:1330 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:35
L:1343 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:36
L:1356 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:37
L:1369 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:38
L:1382 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:39
```